

Jung-Kyung Moon

List of Publications by Year in descending order

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46
papers

2,331
citations

279798

23
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223800

46
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49
all docs

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docs citations

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times ranked

2320
citing authors

#	ARTICLE	IF	CITATIONS
1	Effect of Soybean Volatiles on the Behavior of the Bean Bug, <i>Riptortus pedestris</i> . <i>Journal of Chemical Ecology</i> , 2022, 48, 207-218.	1.8	9
2	The discovery of novel SNPs associated with group A soyasaponin biosynthesis from Korea soybean core collection. <i>Genomics</i> , 2022, 114, 110432.	2.9	4
3	The patterns of deleterious mutations during the domestication of soybean. <i>Nature Communications</i> , 2021, 12, 97.	12.8	49
4	Genome-Wide Association Study for Ultraviolet-B Resistance in Soybean (<i>Glycine max</i> L.). <i>Plants</i> , 2021, 10, 1335.	3.5	7
5	Chromosomal features revealed by comparison of genetic maps of <i>Glycine max</i> and <i>Glycine soja</i> . <i>Genomics</i> , 2020, 112, 1481-1489.	2.9	8
6	High Throughput Phenotyping for Various Traits on Soybean Seeds Using Image Analysis. <i>Sensors</i> , 2020, 20, 248.	3.8	37
7	Genome-wide association and epistatic interactions of flowering time in soybean cultivar. <i>PLoS ONE</i> , 2020, 15, e0228114.	2.5	23
8	Korean soybean core collection: Genotypic and phenotypic diversity population structure and genome-wide association study. <i>PLoS ONE</i> , 2019, 14, e0224074.	2.5	56
9	Growth Response and Developing Simple Test Method for Waterlogging Stress Tolerance in Soybean. <i>Journal of Crop Science and Biotechnology</i> , 2019, 22, 371-378.	1.5	6
10	GmBRC1 is a Candidate Gene for Branching in Soybean (<i>Glycine max</i> (L.) Merrill). <i>International Journal of Molecular Sciences</i> , 2019, 20, 135.	4.1	23
11	Genetic diversity patterns and domestication origin of soybean. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1179-1193.	3.6	44
12	Differences in the metabolic profiles and antioxidant activities of wild and cultivated black soybeans evaluated by correlation analysis. <i>Food Research International</i> , 2017, 100, 166-174.	6.2	25
13	GenoCore: A simple and fast algorithm for core subset selection from large genotype datasets. <i>PLoS ONE</i> , 2017, 12, e0181420.	2.5	41
14	Molecular Genetic Analysis of a Novel Recessive White Flower Gene in Wild Soybean. <i>Crop Science</i> , 2017, 57, 3027-3034.	1.8	1
15	Identification of haplotypes at the <i>Rsv4</i> genomic region in soybean associated with durable resistance to soybean mosaic virus. <i>Theoretical and Applied Genetics</i> , 2016, 129, 453-468.	3.6	37
16	Development of a new vector using Soybean yellow common mosaic virus for gene function study or heterologous protein expression in soybeans. <i>Journal of Virological Methods</i> , 2016, 228, 1-9.	2.1	17
17	Optimization of a Virus-Induced Gene Silencing System with Soybean yellow common mosaic virus for Gene Function Studies in Soybeans. <i>Plant Pathology Journal</i> , 2016, 32, 112-122.	1.7	15
18	Draft genome sequence of adzuki bean, <i>Vigna angularis</i> . <i>Scientific Reports</i> , 2015, 5, 8069.	3.3	144

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19	Development, validation and genetic analysis of a large soybean SNP genotyping array. <i>Plant Journal</i> , 2015, 81, 625-636.	5.7	125
20	Genetic diversity and population structure of wild soybean (<i>Glycine soja</i> Sieb. and Zucc.) accessions in Korea. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2014, 12, S45-S48.	0.8	5
21	Genome-wide comparative analysis of flowering genes between <i>Arabidopsis</i> and mungbean. <i>Genes and Genomics</i> , 2014, 36, 799-808.	1.4	14
22	Genome sequence of mungbean and insights into evolution within <i>Vigna</i> species. <i>Nature Communications</i> , 2014, 5, 5443.	12.8	453
23	Genome-wide single nucleotide polymorphism discovery and validation in adzuki bean. <i>Molecular Breeding</i> , 2014, 33, 497-501.	2.1	22
24	Population Structure and Domestication Revealed by High-Depth Resequencing of Korean Cultivated and Wild Soybean Genomes. <i>DNA Research</i> , 2014, 21, 153-167.	3.4	92
25	Sequence variability in the HC-Pro coding regions of Korean soybean mosaic virus isolates is associated with differences in RNA silencing suppression. <i>Archives of Virology</i> , 2014, 159, 1373-1383.	2.1	14
26	Dynamic genetic features of chromosomes revealed by comparison of soybean genetic and sequence-based physical maps. <i>Theoretical and Applied Genetics</i> , 2013, 126, 1103-1119.	3.6	21
27	Genome-wide SNP discovery in mungbean by Illumina HiSeq. <i>Theoretical and Applied Genetics</i> , 2013, 126, 2017-2027.	3.6	37
28	<i>Ln</i> is a Key Regulator of Leaflet Shape and Number of Seeds per Pod in Soybean. <i>Plant Cell</i> , 2013, 24, 4807-4818.	6.6	90
29	Actin Cytoskeleton and Golgi Involvement in Barley stripe mosaic virus Movement and Cell Wall Localization of Triple Gene Block Proteins. <i>Plant Pathology Journal</i> , 2013, 29, 17-30.	1.7	9
30	Sequence Information on Simple Sequence Repeats and Single Nucleotide Polymorphisms through Transcriptome Analysis of Mungbean. <i>Journal of Integrative Plant Biology</i> , 2011, 53, 63-73.	8.5	58
31	Fine genetic mapping of the genomic region controlling leaflet shape and number of seeds per pod in the soybean. <i>Theoretical and Applied Genetics</i> , 2011, 122, 865-874.	3.6	52
32	Novel major quantitative trait loci regulating the content of isoflavone in soybean seeds. <i>Genes and Genomics</i> , 2011, 33, 685-692.	1.4	38
33	RNA-Seq Analysis of a Soybean Near-Isogenic Line Carrying Bacterial Leaf Pustule-Resistant and -Susceptible Alleles. <i>DNA Research</i> , 2011, 18, 483-497.	3.4	96
34	Genetic Analysis of Genes Controlling Natural Variation of Seed Coat and Flower Colors in Soybean. <i>Journal of Heredity</i> , 2010, 101, 757-768.	2.4	84
35	Whole-genome sequencing and intensive analysis of the undomesticated soybean (<i>Glycine soja</i>) Tj ETQq1 1 0.784314 rgBT /Ove America, 2010, 107, 22032-22037.	7.1	299
36	Nucleotide sequence and genomic organization of a newly identified member of the genus Carmovirus, soybean yellow mottle mosaic virus, from soybean. <i>Archives of Virology</i> , 2009, 154, 1679-1684.	2.1	30

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37	Marker-assisted identification of resistance genes to soybean mosaic virus in soybean lines. <i>Euphytica</i> , 2009, 169, 375-385.	1.2	16
38	Genetic analysis of new short petiole gene in soybean. <i>Journal of Crop Science and Biotechnology</i> , 2009, 12, 87-89.	1.5	11
39	Genome structure in soybean revealed by a genomewide genetic map constructed from a single population. <i>Genomics</i> , 2008, 92, 52-59.	2.9	18
40	Developmental Characteristics of Soybean Podworm, <i>Matsumuraesia phaseoli</i> (Lepidoptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 627 Diets. <i>Korean Journal of Applied Entomology</i> , 2007, 46, 393-399.	0.3	16
41	Application of comparative genomics in developing molecular markers tightly linked to the virus resistance gene <i>Rsv4</i> in soybean. <i>Genome</i> , 2006, 49, 380-388.	2.0	54
42	Bacterial Common Blight and Fuscos Blight of Small Red Bean caused by <i>Xanthomonas axonopodis</i> pv. <i>phaseoli</i> and <i>X. axonopodis</i> pv. <i>phaseoli</i> var. <i>fuscans</i> . <i>Research in Plant Disease</i> , 2006, 12, 129-133.	0.8	1
43	First Report of Soybean Dwarf Virus on Soybean(<i>Glycine max</i>) in Korea. <i>Research in Plant Disease</i> , 2006, 12, 213-220.	0.8	3
44	SNP identification and SNAP marker development for a <i>GmNARK</i> gene controlling supernodulation in soybean. <i>Theoretical and Applied Genetics</i> , 2005, 110, 1003-1010.	3.6	54
45	Identification of Soybean mosaic virus Strains by RT-PCR/RFLP Analysis of Cylindrical Inclusion Coding Region. <i>Plant Disease</i> , 2004, 88, 641-644.	1.4	13
46	G7H, a New Soybean mosaic virus Strain: Its Virulence and Nucleotide Sequence of CI Gene. <i>Plant Disease</i> , 2003, 87, 1372-1375.	1.4	49